



## SEQUENCE LISTING

&lt;110&gt; WISCONSIN ALUMNI RESEARCH FOUNDATION

&lt;120&gt; E. COLI O157:H7 C1 ESTERASE INHIBITOR-BINDING PROTEIN AND METHODS OF USE

&lt;130&gt; 096429-9117

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&lt;160&gt; 17

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 2798

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Description of Unknown Organism: E. coli O157:H7 plasmid pO157

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (138)..(2798)

&lt;223&gt;

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agagatggag aacaccg atg aaa tta aag tat ctg tca tgt acg atc ctt 170

Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu  
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gcc cct ctg gcg att ggg gta ttt tct gca aca gct gct gat aat aat 218

Ala Pro Leu Ala Ile Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn  
15 20 25

tca gcc att tat ttc aat acc tcc cag cct ata aat gat ctg cag ggt 266

Ser Ala Ile Tyr Phe Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly  
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tcg ttg gcc gca gag gtg aaa ttt gca caa agc cag att tta ccc gcc 314

Ser Leu Ala Ala Glu Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala  
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cat cct aaa gaa ggg gat agt caa cca cat ctg acc agc ctg cgg aaa 362

His Pro Lys Glu Gly Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys  
60 65 70 75

agt ctg ctg ctt gtc cgt ccg gtg aaa gct gat gat aaa aca cct gtt 410

Ser Leu Leu Leu Val Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val  
80 85 90

cag gtg gaa gcc cgc gat gat aat aat aaa att ctc ggt acg tta acc 458

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APR 24 2002  
TECH CENTER 1600/2900

Gln Val Glu Ala Arg Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr	
95 100 105	
ctt tat cct cct tca tca cta ccg gat aca atc tac cat ctg gat ggt	506
Leu Tyr Pro Pro Ser Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly	
110 115 120	
gtt ccg gaa ggt ggt atc gat ttc aca cct cat aat gga acg aaa aag	554
Val Pro Glu Gly Gly Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys	
125 130 135	
atc att aat acg gtg gct gaa gta aac aaa ctc agt gat gcc agc ggg	602
Ile Ile Asn Thr Val Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly	
140 145 150 155	
agt tct att cat agc cat cta aca aat aat gca ctg gtg gag atc cat	650
Ser Ser Ile His Ser His Leu Thr Asn Asn Ala Leu Val Glu Ile His	
160 165 170	
act gca aat ggt cgt tgg gta aga gac att tat ctg ccg cag gga ccc	698
Thr Ala Asn Gly Arg Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro	
175 180 185	
gac ctt gaa ggt aag atg gtt cgc ttt gtt tcg tct gca ggc tat agt	746
Asp Leu Glu Gly Lys Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser	
190 195 200	
tca acg gtt ttt tat ggt gat cga aaa gtc aca ctc tcg gtg ggt aac	794
Ser Thr Val Phe Tyr Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn	
205 210 215	
act ctt ctg ttc aaa tat gta aat ggt cag tgg ttc cgc tcc ggt gaa	842
Thr Leu Leu Phe Lys Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu	
220 225 230 235	
ctg gag aat aat cga atc act tat gct cag cat att tgg agt gct gaa	890
Leu Glu Asn Asn Arg Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu	
240 245 250	
ctg cct gcg cac tgg atc gtg cct ggt tta aac ttg gtg att aaa cag	938
Leu Pro Ala His Trp Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln	
255 260 265	
ggc aat ctg agc ggt cgc cta aat gat atc aag att gga gca ccg ggt	986
Gly Asn Leu Ser Gly Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly	
270 275 280	
gag ctg ttg ttg cat aca att gat atc ggg atg ttg acc act ccc cgg	1034
Glu Leu Leu Leu His Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg	
285 290 295	
gat cgc ttt gat ttt gcc aaa gac aaa gaa gca cat agg gaa tat ttc	1082
Asp Arg Phe Asp Phe Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe	
300 305 310 315	
cag acc att cct gta agt cgt atg att gtt aat aat tat gcg cct cta	1130
Gln Thr Ile Pro Val Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu	
320 325 330	
cac cta aag gaa gtt atg tta cca acc gga gag tta ttg aca gat atg	1178
His Leu Lys Glu Val Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met	
335 340 345	

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aat agt acc gca ggc tta ggg gag aat agt cat cca tat gta gtt gcg Asn Ser Thr Ala Gly Leu Gly Glu Asn Ser His Pro Tyr Val Val Ala 380 385 390 395	1322
caa tta gcg gca cat aat agc cgc ggt aat tat gct aat ggc atc cag Gln Leu Ala Ala His Asn Ser Arg Gly Asn Tyr Ala Asn Gly Ile Gln 400 405 410	1370
gtt cat ggt ggc tcc gga ggt ggg gga att gtt act tta gat tcc aca Val His Gly Gly Ser Gly Gly Gly Ile Val Thr Leu Asp Ser Thr 415 420 425	1418
ttg ggg aat gag ttc agt cat gaa gtt ggt cat aat tat ggt ctt ggt Leu Gly Asn Glu Phe Ser His Glu Val Gly His Asn Tyr Gly Leu Gly 430 435 440	1466
cat tat gta gat ggt ttc aag ggt tct gta cat cgt agt gca gaa aat His Tyr Val Asp Gly Phe Lys Gly Ser Val His Arg Ser Ala Glu Asn 445 450 455	1514
aac aac tca act tgg gga tgg gat ggt gat aaa aaa cgg ttt att cct Asn Asn Ser Thr Trp Gly Trp Asp Gly Asp Lys Lys Arg Phe Ile Pro 460 465 470 475	1562
aac ttt tat ccg tct caa aca aat gaa aag agt tgt ctg aat aat cag Asn Phe Tyr Pro Ser Gln Thr Asn Glu Lys Ser Cys Leu Asn Asn Gln 480 485 490	1610
tgt caa gaa ccg ttt gat gga cac aaa ttt ggt ttt gac gcc atg gcg Cys Gln Glu Pro Phe Asp Gly His Lys Phe Gly Phe Asp Ala Met Ala 495 500 505	1658
gga ggc agc cct ttc tct gct gca aac cgt ttc aca atg tat act ccg Gly Gly Ser Pro Phe Ser Ala Ala Asn Arg Phe Thr Met Tyr Thr Pro 510 515 520	1706
aat tca tgc gct atc atc cag cgt ttt ttt gaa aat aaa gct gtg ttc Asn Ser Ser Ala Ile Ile Gln Arg Phe Phe Glu Asn Lys Ala Val Phe 525 530 535	1754
gat agc cgt tcc tcc acc ggc ttc agc aag tgg aat gca gat acg cag Asp Ser Arg Ser Ser Thr Gly Phe Ser Lys Trp Asn Ala Asp Thr Gln 540 545 550 555	1802
gaa atg gaa ccg tat gaa cac acc att gac cgt gcg gag cag att acg Glu Met Glu Pro Tyr Glu His Thr Ile Asp Arg Ala Glu Gln Ile Thr 560 565 570	1850
gct tca gtc aat gag cta agt gaa agc aaa atg gct gag ctg atg gca Ala Ser Val Asn Glu Leu Ser Glu Ser Lys Met Ala Glu Leu Met Ala 575 580 585	1898
gag tac gct gtc gtc aaa gtg cat atg tgg aac ggt aac tgg aca aga	1946

Glu Tyr Ala Val Val Lys Val His Met Trp Asn Gly Asn Trp Thr Arg	
590 595 600	
aac atc tat atc cct aca gcc tcc gca gat aat aga ggc agt atc ctg	1994
Asn Ile Tyr Ile Pro Thr Ala Ser Ala Asp Asn Arg Gly Ser Ile Leu	
605 610 615	
acc atc aac cat gag gcc ggt tat aat agt tat ctg ttt ata aat ggt	2042
Thr Ile Asn His Glu Ala Gly Tyr Asn Ser Tyr Leu Phe Ile Asn Gly	
620 625 630 635	
gac gaa aag gtc gtt tcc cag ggg tat aaa aag agc ttt gtt tcc gat	2090
Asp Glu Lys Val Val Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp	
640 645 650	
ggg cag ttc tgg aaa gaa cgt gat gtg gtt gat act cgt gaa gcg cgt	2138
Gly Gln Phe Trp Lys Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg	
655 660 665	
aag cca gag cag ttt ggt gtt cct gtg acg acc ctg gtg ggg tat tac	2186
Lys Pro Glu Gln Phe Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr	
670 675 680	
gat ccg gaa ggc acg ctg tca agc tac atc tat cct gcg atg tat ggt	2234
Asp Pro Glu Gly Thr Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly	
685 690 695	
gcc tat ggc ttc act tat tcc gat gat agt cag aat cta tcc gat aac	2282
Ala Tyr Gly Phe Thr Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn	
700 705 710 715	
gac tgc cag ctg cag gtg gat acg aaa gaa ggg cag ttg cga ttc aga	2330
Asp Cys Gln Leu Gln Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg	
720 725 730	
ctg gct aat cac cgg gct aac aac act gta atg aat aag ttc cat att	2378
Leu Ala Asn His Arg Ala Asn Asn Thr Val Met Asn Lys Phe His Ile	
735 740 745	
aac gtg cca aca gaa agt cag ccc aca cag gcc aca ttg gtt tgc aat	2426
Asn Val Pro Thr Glu Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn	
750 755 760	
aac aag ata ctg gat acc aaa tcg ctc aca cct gcg cca gaa gga ctt	2474
Asn Lys Ile Leu Asp Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu	
765 770 775	
acc tat act gta aat ggg cag gca ctt cca gca aaa gaa aac gag gga	2522
Thr Tyr Thr Val Asn Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly	
780 785 790 795	
tgc atc gtg tcc gtg aat tca ggt aaa cgt tac tgt ttg ccg gtt ggt	2570
Cys Ile Val Ser Val Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly	
800 805 810	
caa cgg tca gga tat agc ctt cct gac tgg att gtt ggg cag gaa gtc	2618
Gln Arg Ser Gly Tyr Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val	
815 820 825	
tat gtc gac agc ggg gct aaa gcg aaa gtg ctg ctt tct gac tgg gat	2666
Tyr Val Asp Ser Gly Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp	
830 835 840	

aac ctg tcc tat aac agg att ggt gag ttt gta ggt aat gtg aac cca 2714  
 Asn Leu Ser Tyr Asn Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro  
 845 850 855

gct gat atg aaa aaa gtt aaa gcc tgg aac gga cag tat ttg gac ttc 2762  
 Ala Asp Met Lys Lys Val Lys Ala Trp Asn Gly Gln Tyr Leu Asp Phe  
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agt aaa cct agg tca atg agg gtt gta tat aaa taa 2798  
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 <223> Description of Unknown Organism: E. coli O157:H7 plasmid pO157

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Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly Ser Leu Ala Ala Glu  
 35 40 45

Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala His Pro Lys Glu Gly  
 50 55 60

Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys Ser Leu Leu Leu Val  
 65 70 75 80

Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val Gln Val Glu Ala Arg  
 85 90 95

Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr Leu Tyr Pro Pro Ser  
 100 105 110

Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly Val Pro Glu Gly Gly  
 115 120 125

Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys Ile Ile Asn Thr Val  
 130 135 140

Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly Ser Ser Ile His Ser  
 145 150 155 160

His Leu Thr Asn Asn Ala Leu Val Glu Ile His Thr Ala Asn Gly Arg  
 165 170 175

Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro Asp Leu Glu Gly Lys  
 180 185 190

Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser Ser Thr Val Phe Tyr  
 195 200 205

Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn Thr Leu Leu Phe Lys  
 210 215 220

Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu Leu Glu Asn Asn Arg  
 225 230 235 240

Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu Leu Pro Ala His Trp  
 245 250 255

Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln Gly Asn Leu Ser Gly  
 260 265 270

Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly Glu Leu Leu Leu His  
 275 280 285

Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg Asp Arg Phe Asp Phe  
 290 295 300

Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe Gln Thr Ile Pro Val  
 305 310 315 320

Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu His Leu Lys Glu Val  
 325 330 335

Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met Asp Pro Gly Asn Gly  
 340 345 350

Gly Trp His Ser Gly Thr Met Arg Gln Arg Ile Gly Lys Glu Leu Val  
 355 360 365

Ser His Gly Ile Asp Asn Ala Asn Tyr Gly Leu Asn Ser Thr Ala Gly  
 370 375 380

Leu Gly Glu Asn Ser His Pro Tyr Val Val Ala Gln Leu Ala Ala His  
 385 390 395 400

Asn Ser Arg Gly Asn Tyr Ala Asn Gly Ile Gln Val His Gly Gly Ser  
 405 410 415  
 Gly Gly Gly Gly Ile Val Thr Leu Asp Ser Thr Leu Gly Asn Glu Phe  
 420 425 430  
 Ser His Glu Val Gly His Asn Tyr Gly Leu Gly His Tyr Val Asp Gly  
 435 440 445  
 Phe Lys Gly Ser Val His Arg Ser Ala Glu Asn Asn Asn Ser Thr Trp  
 450 455 460  
 Gly Trp Asp Gly Asp Lys Lys Arg Phe Ile Pro Asn Phe Tyr Pro Ser  
 465 470 475 480  
 Gln Thr Asn Glu Lys Ser Cys Leu Asn Asn Gln Cys Gln Glu Pro Phe  
 485 490 495  
 Asp Gly His Lys Phe Gly Phe Asp Ala Met Ala Gly Gly Ser Pro Phe  
 500 505 510  
 Ser Ala Ala Asn Arg Phe Thr Met Tyr Thr Pro Asn Ser Ser Ala Ile  
 515 520 525  
 Ile Gln Arg Phe Phe Glu Asn Lys Ala Val Phe Asp Ser Arg Ser Ser  
 530 535 540  
 Thr Gly Phe Ser Lys Trp Asn Ala Asp Thr Gln Glu Met Glu Pro Tyr  
 545 550 555 560  
 Glu His Thr Ile Asp Arg Ala Glu Gln Ile Thr Ala Ser Val Asn Glu  
 565 570 575  
 Leu Ser Glu Ser Lys Met Ala Glu Leu Met Ala Glu Tyr Ala Val Val  
 580 585 590  
 Lys Val His Met Trp Asn Gly Asn Trp Thr Arg Asn Ile Tyr Ile Pro  
 595 600 605  
 Thr Ala Ser Ala Asp Asn Arg Gly Ser Ile Leu Thr Ile Asn His Glu  
 610 615 620  
 Ala Gly Tyr Asn Ser Tyr Leu Phe Ile Asn Gly Asp Glu Lys Val Val  
 625 630 635 640  
 Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp Gly Gln Phe Trp Lys  
 645 650 655

Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg Lys Pro Glu Gln Phe  
660 665 670

Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr Asp Pro Glu Gly Thr  
675 680 685

Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly Ala Tyr Gly Phe Thr  
690 695 700

Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn Asp Cys Gln Leu Gln  
705 710 715 720

Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg Leu Ala Asn His Arg  
725 730 735

Ala Asn Asn Thr Val Met Asn Lys Phe His Ile Asn Val Pro Thr Glu  
740 745 750

Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn Asn Lys Ile Leu Asp  
755 760 765

Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu Thr Tyr Thr Val Asn  
770 775 780

Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly Cys Ile Val Ser Val  
785 790 795 800

Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly Gln Arg Ser Gly Tyr  
805 810 815

Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val Tyr Val Asp Ser Gly  
820 825 830

Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp Asn Leu Ser Tyr Asn  
835 840 845

Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro Ala Asp Met Lys Lys  
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Met Arg Val Val Tyr Lys  
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<210> 3  
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<220>  
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 <223> Description of Unknown Organism: E. coli O157:H7 plasmid pO157

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 <211> 28  
 <212> DNA  
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 <212> DNA  
 <213> Synthetic Oligonucleotide

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 <212> DNA  
 <213> Synthetic Oligonucleotide

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 <211> 27  
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 <212> DNA  
 <213> Synthetic Oligonucleotide

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<210> 9

<211> 30  
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<400> 9  
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<400> 10  
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 <212> DNA  
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<210> 17  
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